**Figure 1**

adh_short: domain 1/1, from 37 to 249: score 135.6, E=9.1e-37

```

Begin SEQ ID NO:7 *-> KvalVTGassGIGlaiAkrLakeGakVvvadrneeklekG.....
+v+L+Tga+sG+G+ A++++a+ a +v+ d+n e+ + ++
SEQ ID NO:2 (21617) 37 QVCLITGAGSGLGRLFALEFARRRALLVLWDINTQSNEETagmvrhi 83

.....avakelkelGnd.....kdralaiqlDvtdeesvkaaveqav
++ +a+ +++ ++G++ ++ ++ ++++++Dv ++e v ++e+++
21617 84 yrdleAADAALQAGNGEeeilphcNLQVFTYTCDVGKRENVYLTAERV 133

erlGrGlDvLVNNAGgiillrpgpfaelsrtneedwdrvidvNltgvfll
+++G + vLVNNAG + + ++e + +e+++r++ vN ++ f++
21617 134 KEVGE-VSVLVNNAG--V-VSGHLLLECP---DELIERTMMVNCCHAHFWT 176

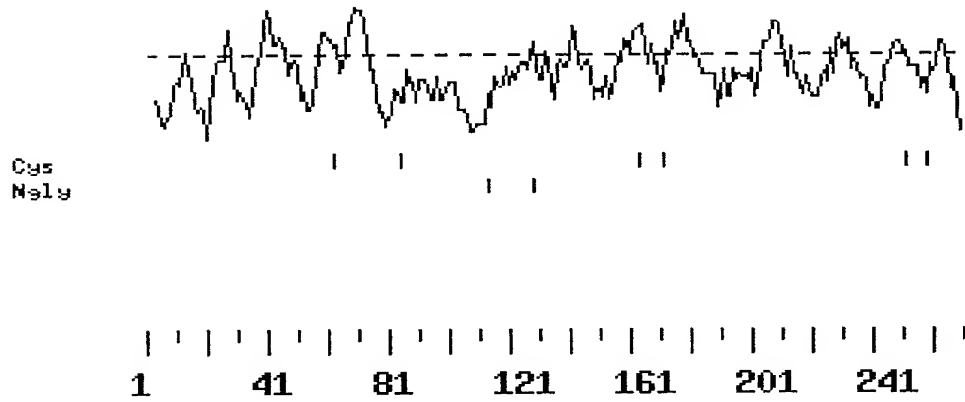
travlpImamkkrGgGrIvNiSSvaGrkegglvvpgggsaYsASKaAavig
t+a+lp m++ +G Iv+++S G 1 +g Y+ASK++v+g
21617 177 TKAFLP--TMLEINHGHIVTVASSLG-----LFSTAGVEDYCASKFGVVG 219

ltrsLAlElaphg..gIrVnavaPGgvdTd <-* End SEQ ID NO:7
+ +sL +El+ ++gI+ v+p vdt
21617 220 FHESLSHELKAAEkdgIKTTLVCPYLVDTG 249 SEQ ID NO:2

```

Figure 2

Applicant(s): Rajasekhar Bandaru, et al.

55562 AND 21617, NOVEL HUMAN PROTEINS AND
METHODS OF USE THEREOF**Figure 3**

TPR: domain 1 of 1, from 40 to 73: score 7.5, E = 7.2

```

Begin SEQ ID NO:8 *-> aeayynlGnaylklgkydeAiedyekALeIdPnn <-* End SEQ ID NO:8
a + +++ + + +Y +A+ +Y++ ++1 +
SEQ ID NO:5 (55562) 40 AATVLKRAVELDSESRYPQALVCYQEGIDLLQV 73

```

Figure 4

PD314595 p2001.1 (1)

Score = 386 (140.9 bits), Expect = 6.8e-36, P = 6.8e-36
Identities = 80/228 (35%), Positives = 126/228 (55%)

```
Begin SEQ ID NO:9 *-> AKELLIRAVECDQVGRILEAQTLYTEGIGQLMQFVNGEPDEAKRGFLTRIKEYMDRADA
                        A +L RAVE D R +A Y EGI L+Q + G D KR +I +YMDRA+
SEQ ID NO:5 (55562) 40 AATVLKRAVELDSESRYPALVCYQEGIDLLQLKGTCDNTKRCNLREKISKYMDRAEN 99

                        IKARINGKMLGEVVSHVSIDENDTGFDYDQLFGKYMDDDKTVEIMLEEPYMTQNYQYNL
IK ++ + G+ + I+EN TGF Y+ LF +Y+++ E+ +E+PY+ +Q N
55562 100 IKKYLDQEKEDGKYHKQIKIEENATGFSYESLFRAYLNETVTVEVWIEDPYIRHTHQLYNF 159

                        IRFLELAATNCPNLKYFRLITKEYKDAKNPDQQETNLGQIKGDLERRNVTVYIKYEDSLH
+RF E+ +K L+T + QQ L +I+ L V + ++Y S+H
55562 160 LRFCEMLIKRPFCKVKTIHLLTS-LDEGIEQVQQSRGLQEI EESLRSHGVLLLEVQYSSSIH 218

                        DRKIYLSNGYIIKIGRGLHFYKPPANPMYSIGLVNYKFRKCLQTDVDIW <-* End SEQ ID NO:9
DR+I +NG++IKIGRGL ++K +S+G ++ R C +T VDI+
55562 219 DREIRFNNGWMIKIGRGLDYFKKPQSRFSLGYCYCDFDLRPFCHETTVDF 266 SEQ ID NO:2
```

Figure 5

PD014461 p99.2 (4)

Score = 84 (34.6 bits), Expect = 0.0019, P = 0.0019
Identities = 18/59 (30%), Positives = 32/59 (54%)

Begin SEQ ID NO:10 *-> AIDL VQKAIDEDKAGQYEEAYQLYQHALDYFMHALKYEAKNDKSKEIIRAKC
A ++++A++ D +Y +A YQ +D + LK N K + R K
SEQ ID NO:5 (55562) 40 AATVLKRAVELDSESRYPQALVCYQEGIDLLQLVKGTKDNTKRCNL-REKI 90

TEYLDRA <-* End SEQ ID NO:10
++Y+DRA
55562 91 SKYMDRA 97 SEQ ID NO:5

Figure 6